



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/623,746 (Pct)
Source: PCT
Date Processed by STIC: 2-5-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT.

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/623, 746

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply
Corrected Diskette Needed

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/623,746

DATE: 02/05/2001

TIME: 16:30:26

Input Set : A:\PTO.txt

Output Set: N:\CRF3\02052001\I623746.raw

5 <110> APPLICANT: metaGen Gesellschaft for Genomforschung mbH
7 <120> TITLE OF INVENTION: Menschliche Nukleins uresequenzen aus Prostatagewebe
9 <130> FILE REFERENCE: 51570AWOM1XX24-P
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/623,746
C--> 12 <141> CURRENT FILING DATE: 2000-09-08
14 <160> NUMBER OF SEQ ID NOS: 295

→ English
translation
please.

ERRORED SEQUENCES

1640 <210> SEQ ID NO: 83
1641 <211> LENGTH: 148
1642 <212> TYPE: PRT
1643 <213> ORGANISM: homo sapiens
1645 <400> SEQUENCE: 83
1647 Glu Ala Ala Leu Thr Leu Cys His Leu Leu Ser Ser Trp Val Ser Leu
1648 1 5 10 15
1650 Glu Ser Leu Thr Leu Ser Tyr Asn Gly Leu Gly Ser Asn Ile Phe Arg
1651 20 25 30
1653 Leu Leu Asp Ser Leu Arg Ala Leu Ser Gly Gln Ala Gly Cys Arg Leu
1654 35 40 45
1656 Arg Ala Leu His Leu Ser Asp Leu Phe Ser Pro Leu Pro Ile Leu Glu
1657 50 55 60
1659 Leu Thr Arg Ala Ile Val Arg Ala Leu Pro Leu Leu Arg Val Leu Ser
1660 65 70 75 80
1662 Ile Arg Val Asp His Pro Ser Gln Arg Asp Asn Pro Gly Val Pro Gly
1663 85 90 95
1665 Asn Ala Gly Pro Pro Ser His Ile Ile Gly Asp Glu Glu Ile Pro Glu
1666 100 105 110
E--> 1668 Asn Cys Leu Glu Gln Leu Glu Met Xxx Ile Ser Thr Gly Ser Pro Ala
1669 115 120 125
1671 Ser Pro Thr Ala Val Leu Arg Ser Glu Gly Leu Gly Phe Ser Ala Ala
1672 130 135 140
1674 Ala Val Pro Gly
1675 145
3782 <210> SEQ ID NO: 203
3783 <211> LENGTH: 66
3784 <212> TYPE: PRT
3785 <213> ORGANISM: homo sapiens
3787 <400> SEQUENCE: 203
E--> 3789 Ser Pro Gly Phe Phe Leu Ser Leu Pro Phe Ser Thr Gly Xxx Ala Trp
3790 1 5 10 15
3792 Ala Ser Ser Ser Cys His Pro Ser Arg Lys Ala Pro Ala Pro Ser Cys
3793 20 25 30
3795 Leu Pro Ala Ala Cys Ile Gln Gly Gln Ser Ser Gly Leu Gln Thr Gly
3796 35 40 45
3798 Leu Val Pro Pro Pro Leu Gln Gly Met Gly Val Gly Glu Gly Ala Phe

missing mandatory <220> to <223> features
to explain Xaa in the sequence. See #10
on the Error
Summary Sheet.

Invalid amino acid designator.
(Xaa?)

Seq. #203 also is missing the <220> to <223>
feature to explain the Xaa in the sequence.
All sequences with "n's" or "Xaa's" must have
the <220> to <223> features.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/623,746
 DATE: 02/05/2001
 TIME: 16:30:26

Input Set : A:\PTO.txt
 Output Set : N:\CRF3\02052001\I623746.raw

```

3799          50          55          60
3801      Lys  Lys
3802      65
4152 <210> SEQ ID NO: 220
4153 <211> LENGTH: 3210
4154 <212> TYPE: DNA
4155 <213> ORGANISM: homo sapiens
4157 <400> SEQUENCE: 220
4159 gcaaggccta ctgtcgctg ggaggggagg tgtagccggt ctttgggggt aggcggtagt 60
4160 ggcggaagag gttcggcggc tgatggcgga tcaggatcgg aagcctgcgt aactttctcc 120
4161 cttgatccgg gagtctttcc actggattca caatgacatc ctttcaagaa gtcccaattgc 180
4162 agacttccaa ctttgcctat gtcattcttc aaaaatgtgc caagaattac ctctctaattg 240
4163 cacacctgga atgtcattac accttaactc catatatcca tccacatcca aaagattggg 300
4164 ttggtatatt caaggttggg tggagtactg ctctgtgatta ttacacgttt ttatggtecc 360
4165 ctatgcctga acattatgtg gaaggatcaa cagtcaattg tgtactagca ttccaaggat 420
4166 attaccttcc aaatgatgat ggagaatttt atcagttctg ttacgtttacc cataagggtg 480
4167 aaattcgtgg agcaagtaca cctttccagt ttctgagctt ttctccagtt gaagagctgc 540
4168 ttactatgga agatgaagga aattctgaca tgttagtggt gaccacaaaa gcaggccttc 600
4169 ttgagttgaa aattgagaaa accatgaaag aaaaagaaga actgttaaa ttaattgcgc 660
4170 ttctggaaaa aqaaaacaca caacttcgag aacaagttag gagaatggaa agagaactta 720
4171 accatgagaa agaaagatgt gaccaactgc aagcagaaca aaaggtctt actgaagtaa 780
4172 cacaaagctt aaaaatggaa aatgaagagt ttaagaagag gttcagtgat gctacatcca 840
4173 aagcccatca gcttgaggaa gatatttgtt cagttaacaca taaagcaatt gaaaaagaaa 900
E--> 4174 cgaattaga cagtttaaa gacaaactca agaaggcaca acatgaaaga gaacaacttg 960
E--> 4175 aatgtcagtt gaagacagag aaggatgaaa aggaacttta taaggtagat ttgaagaata 1020
E--> 4176 cagaaataga aaataccaag cttatgtcag aggtccagac tttaaaaaat ttagatggga 1080
E--> 4177 acaaagaaag cgtgattact catttcaaa aagagattgg caggctgcag ttatgtttgg 1140
E--> 4178 ctgaaaagga aaatctgcaa agaactttcc tgcttacaac ctcaagtaaa gaagatactt 1200
E--> 4179 gtttttttaa ggagcaactt cgtaaagcag aggaacaggt tcaggcaact cggcaagaag 1260
E--> 4180 ttgtctttct ggctaaagaa ctcagtgatg ctgtcaacgt acgagacaga acgatggcag 1320
E--> 4181 acctgcatac tgcacgcttg gaaaacgaga aagtgaaaaa gcagttagct gatgcagtg 1380
E--> 4182 cagaacttaa actaaatgct atgaaaaaag atcaggacaa gactgatata ctggaacacg 1440
E--> 4183 aactaagaag agaagttgaa gatctgaaac tccgtcttca gatggctgca gaccattata 1500
E--> 4184 aagaaaaatt taaggaatgc caaaggctcc aaaaacaaat aaacaaactt tcagatcaat 1560
E--> 4185 cagctaataa taataatgtc ttcacaaaga aaacggggaa tcagcagaaa gtgaatgatg 1620
E--> 4186 cttcagtaaa cacagaccca gccacttctg cctctactgt agatgtaaa ccatcacctt 1680
E--> 4187 ctgcagcaga ggcagatttt gacatagtaa caaaggggca agtctgtgaa atgaccaaag 1740
E--> 4188 aaattgctga caaacacaga aagtataata aatgtaaaca actcttgtag gatgagaaag 1800
E--> 4189 caaaatgcaa taaatatgct gatgaacttg caaaaatgga gctgaaatgg aaagaacaag 1860
E--> 4190 tgaaaattgc tgaaaatgta aaacttgaac tagctgaagt acaggacaat tataaagaac 1920
E--> 4191 ttaaaaggag tctagaaaa ccagcagaaa ggaatggaga agatggagca gatgggtgct 1980
E--> 4192 tttaccacga tgaatacaca aggccacctg tcagagtccc ctcttgggga ctggaagaca 2040
E--> 4193 atgttgtctg cagccagcct gctcgaaact ttagtgcggc tgatggctta gaggactctg 2100
E--> 4194 aggatagcaa agaagatgag aatgtgccta ctgctcctga tcctccaagt caacatttac 2160
E--> 4195 gtgggcatgg gacaggcttt tgctttgatt ccagctttga tgttcacaag aagtgtcccc 2220
E--> 4196 tctgtgagtt aatgtttcct cctaactatg atcagagcaa atttgaagaa catgttgaaa 2280
E--> 4197 tgctactggaa ggtgtgcccg atgtgcagcg agcagttccc tctgactatg gaccagcagg 2340
E--> 4198 gtgttgaaag gcatgtgcag acccattttg atcagaatgt tctaaatttt gactagttac 2400
E--> 4199 tttttattat gagttaatat agtttagcag taaaaaaaaa aaaaaaaac cacaccttaa 2460

```

→ only 959 bases
on this line

All following counts
are now errored
due to miscount

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Input Set : A:\PTO.txt
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```

E--> 4200 atagaccact gaggagacca tagageggat gctttcatgc accctttact gcactttctg2520
E--> 4201 accaggagct actttgagtt tgggtgttact aggatcaggg tcagtccttg gcttatcaat2580
E--> 4202 aaattttaat ctctgttaat cttacctgct ttaaaaaaaaaa gttcttgtgt gttcgtatct2640
E--> 4203 ttattttatc cctagtttgc agaactgtct gaataaaggga tacaaggatt atttcaatgt2700
E--> 4204 tactgcactg aaaaacgtgt atgtattagt gtgctagatt atttagcaga atattcacaa2760
E--> 4205 gtttctgttg accttgttga ttgagcatga ctactaaata ttatgtaata aaaagcattt2820
E--> 4206 gtcataacag tcttatgaag tagttcttcg aatatagaaa gttctataat ttagcccatg2880
E--> 4207 aaatgatagg ttttttaatt tcagaaatgg agctgcatgt agaatgagat cacatgcttt2940
E--> 4208 tatatgtgaa atattggttt tagcaattaa cagaaggcat actttgctaa ttttatggca3000
E--> 4209 aaattttaga ataacctgaa tgattatttt taaactatct tgaagttgta tgtatatatc3060
E--> 4210 ctaatggggg aatggggcaa gggattgtca gtataattgt tttcccatt aaatgggtccc3120
E--> 4211 cataaccagg ggggtgtttg gccataaaaa tccatagggg atatagcagg accctttttg3180
E--> 4212 catttccctg tggggattta atttgaatt 3210

```

5998 <210> SEQ ID NO: 261

5999 <211> LENGTH: 196

6000 <212> TYPE: PRT

6001 <213> ORGANISM: homo sapiens

6003 <400> SEQUENCE: 261

6005 Pro Gln Thr Thr Gln Cys Val Arg Arg Ala Gly Leu Trp Val Asn Ser

6006 1 5 10 15

6008 His Ile His Thr Gln Gly Arg Gly Lys His Thr Gln Val Gln Ser Ser

6009 20 25 30

6011 Gln Trp Cys Arg Pro Asp Leu Leu Ser Arg Gly Cys Tyr Gly Cys Pro

6012 35 40 45

6014 Ser Ala Ser Pro Glu Gln Pro Gly Gln Pro Ala Pro Pro Pro Arg Leu

6015 50 55 60

E--> 6017 **Xxx** Gln Glu Gly Glu Leu Cys Pro Gly Glu Glu Thr Asp Arg Leu Gly

6018 65 70 75 80

6020 Asp Lys Thr Pro Ile Ala Gly Thr Cys Thr Ala Ala Ala Thr Ala Pro

6021 85 90 95

6023 Arg Thr Gly His Gly Asp Gly Thr Gly Arg Glu Pro His Cys Pro Leu

6024 100 105 110

6026 Ser Val Cys Leu Trp Phe Cys Pro Gly Pro Ala His Leu Glu Pro Arg

6027 115 120 125

6029 Gln Thr Gly Gly Ile Glu Gln Gly Pro Gly Pro Asp Ser Pro Leu Ala

6030 130 135 140

6032 Arg Cys Asp Trp Lys Arg Leu Met Pro Gly Gln His Gln Ala Phe Cys

6033 145 150 155 160

6035 Lys Ser Gln Ser Gln Cys Ala Glu Ser Ala Ser Thr Ala Cys Ala Val

6036 165 170 175

6038 Ala Pro Gln Asp Glu Val Thr Ser Arg Thr Gly Gly Phe Met Gln Thr

6039 180 185 190

6041 His Arg His Cys

6042 195

6044 <210> SEQ ID NO: 262

6045 <211> LENGTH: 190

6046 <212> TYPE: PRT

6047 <213> ORGANISM: homo sapiens

6049 <400> SEQUENCE: 262

No explanation of the Xaa

Xaa? ←

RAW SEQUENCE LISTING

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\02052001\I623746.raw

```

6051 Asp Gln Leu Gly Ser Gly Gly His Phe Ser Leu His Arg Leu Pro Glu
6052 1 5 10 15
6054 Gln Thr Glu Glu Ser Ser Leu Ile Val Ala Glu Pro Ser Leu Ser Pro
6055 20 25 30
6057 Ser Ala Val Ser Val Cys Leu His Lys Pro Ser Cys Pro Gly Arg Asp
6058 35 40 45
6060 Phe Ile Leu Arg Ser His Ser Thr Gly Arg Ala Gly Thr Phe Cys Thr
6061 50 55 60
6063 Leu Ala Leu Gly Leu Ala Glu Gly Leu Val Leu Pro Trp His Gln Pro
6064 65 70 75 80
6066 Leu Pro Val Thr Ser Gly Gln Arg Ala Val Trp Thr Trp Ala Leu Leu
6067 85 90 95
6069 Asn Ala Thr Cys Leu Pro Gly Leu Gln Val Gly Arg Thr Arg Thr Glu
6070 100 105 110
6072 Pro Gln Ala His Thr Glu Gly Ala Val Trp Leu Pro Ala Cys Pro Ile
6073 115 120 125
6075 Pro Met Pro Arg Pro Arg Gly Cys Gly Cys Cys Cys Cys Pro Cys
6076 130 135 140
6078 Asp Gly Ser Leu Val Ser Gln Pro Val Ser Phe Leu Pro Arg Ala Glu
6079 145 150 155 160
E--> 6081 Leu Pro Phe Leu Xxx Glu Ser Gly Arg Arg Cys Arg Leu Ser Trp Leu
6082 165 170 175
6084 Leu Trp Gly Ser Arg Gly Thr Ala Ile Thr Pro Pro Gly Gln
6085 180 185 190
7063 <210> SEQ ID NO: 289
7064 <211> LENGTH: 84
7065 <212> TYPE: PRT
7066 <213> ORGANISM: homo sapiens
7068 <400> SEQUENCE: 289
7070 Ser Thr Arg Pro Arg Glu Arg Arg Asn Arg Ser Val Asp Glu Cys Gln
7071 1 5 10 15
E--> 7073 Leu Ile Asn Val Lys Xxx Arg His Xxx Leu Val Cys Leu Xxx Cys Phe
7074 20 25 30
E--> 7076 Cys Leu Tyr Xxx Gln Pro Asp Xxx Val Ser Xxx Glu Tyr Lys Xxx Trp
7077 35 40 45
E--> 7079 Gly Leu Leu Pro Gln Xxx Leu Phe Xxx Ile Ser Xxx Glu Lys Lys Asn
7080 50 55 60
E--> 7082 Asp Arg Xxx Xxx Gly Xxx Ile Xxx Arg Xxx Ala Arg Phe Xxx Ser Thr
7083 65 70 75 80
E--> 7085 Asn Xxx Asn Xxx
7087 <210> SEQ ID NO: 290
7088 <211> LENGTH: 77
7089 <212> TYPE: PRT
7090 <213> ORGANISM: homo sapiens
7092 <400> SEQUENCE: 290
E--> 7094 Met Ser Xxx Xxx Asp Thr Xxx Trp Cys Val Xxx Ala Val Phe Ala Phe
7095 1 5 10 15
E--> 7097 Thr Xxx Asn Pro Thr Val Phe His Xxx Asn Thr Asn Xxx Gly Xxx Phe
7098 20 25 30

```

*no <220> to <223> explanations
for the "Xaa's" in the sequences.*

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```

E--> 7100   Tyr  Pro  (Xxx)  Leu  Ser  Ser  (Xxx)  Leu  Val  Lys  Lys  Lys  Lys  Met  Ile  Gly
      7101                                     40
E--> 7103  (Xxx) (Xxx) (Xxx)  Glu  Phe  (Xxx)  Gly  Lys  Pro  (Xxx) (Xxx)  Gln  Ala  Leu  (Xxx)  Lys
      7104                                     55
      50
E--> 7106   Ile  (Xxx)  Ser  Trp  (Xxx) (Xxx)  Leu  Thr  Ser  Leu  Pro  (Xxx) (Xxx)
      65                                     70
      75

```

VERIFICATION SUMMARY

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\02052001\I623746.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:18 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1) SEQUENCE:
L:81 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:81 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:81 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:81 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:81 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:106 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:229 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:229 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:229 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:229 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:229 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:244 M:283 W: Missing Blank Line separator, <400> field identifier
L:245 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:304 M:283 W: Missing Blank Line separator, <400> field identifier
L:305 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:386 M:283 W: Missing Blank Line separator, <400> field identifier
L:387 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:415 M:283 W: Missing Blank Line separator, <400> field identifier
L:416 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (22) SEQUENCE:
L:458 M:283 W: Missing Blank Line separator, <400> field identifier
L:459 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE:
L:643 M:283 W: Missing Blank Line separator, <400> field identifier
L:644 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (34) SEQUENCE:
L:709 M:283 W: Missing Blank Line separator, <400> field identifier
L:710 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (38) SEQUENCE:
L:751 M:283 W: Missing Blank Line separator, <400> field identifier
L:752 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE:
L:852 M:283 W: Missing Blank Line separator, <400> field identifier
L:853 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:
L:905 M:283 W: Missing Blank Line separator, <400> field identifier
L:906 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:
L:909 M:283 W: Missing Blank Line separator, <400> field identifier
L:910 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:
L:913 M:283 W: Missing Blank Line separator, <400> field identifier
L:914 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:
L:964 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:52
L:964 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:964 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:964 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:52
L:964 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
L:1013 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:54
L:1013 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:1013 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54

VERIFICATION SUMMARY

DATE: 02/05/2001

PATENT APPLICATION: US/09/623,746

TIME: 16:30:28

Input Set : A:\PTO.txt

Output Set: N:\CRF3\02052001\I623746.raw

L:1013 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:54
L:1013 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:54
L:1044 M:283 W: Missing Blank Line separator, <400> field identifier
L:1045 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:
L:1048 M:283 W: Missing Blank Line separator, <400> field identifier
L:1049 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (57) SEQUENCE:
L:1147 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
L:1147 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61
L:1147 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61
L:1147 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:61
L:1147 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61
L:1245 M:283 W: Missing Blank Line separator, <400> field identifier
L:1246 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (65) SEQUENCE:
L:1426 M:283 W: Missing Blank Line separator, <400> field identifier
L:1427 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (72) SEQUENCE:
L:1578 M:283 W: Missing Blank Line separator, <400> field identifier
L:1579 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:
L:1582 M:283 W: Missing Blank Line separator, <400> field identifier
L:1583 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (77) SEQUENCE:
L:1586 M:283 W: Missing Blank Line separator, <400> field identifier
L:1587 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (78) SEQUENCE:
L:1590 M:283 W: Missing Blank Line separator, <400> field identifier
L:1591 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:
L:1594 M:283 W: Missing Blank Line separator, <400> field identifier
L:1595 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE:
L:1598 M:283 W: Missing Blank Line separator, <400> field identifier
L:1599 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (81) SEQUENCE:
L:1668 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1678 M:283 W: Missing Blank Line separator, <400> field identifier
L:1679 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (84) SEQUENCE:
L:1682 M:283 W: Missing Blank Line separator, <400> field identifier
L:1683 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (85) SEQUENCE:
L:1686 M:283 W: Missing Blank Line separator, <400> field identifier
L:1687 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (86) SEQUENCE:
L:1690 M:283 W: Missing Blank Line separator, <400> field identifier
L:1691 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (87) SEQUENCE:
L:1694 M:283 W: Missing Blank Line separator, <400> field identifier
L:1695 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (88) SEQUENCE:
L:1698 M:283 W: Missing Blank Line separator, <400> field identifier
L:1699 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (89) SEQUENCE:
L:1859 M:283 W: Missing Blank Line separator, <400> field identifier
L:1860 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (94) SEQUENCE:
L:1863 M:283 W: Missing Blank Line separator, <400> field identifier
L:1864 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (95) SEQUENCE:
L:1867 M:283 W: Missing Blank Line separator, <400> field identifier
L:1868 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (96) SEQUENCE:
L:2090 M:283 W: Missing Blank Line separator, <400> field identifier
L:2091 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (106) SEQUENCE:
L:2094 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

DATE: 02/05/2001

PATENT APPLICATION: US/09/623,746

TIME: 16:30:28

Input Set : A:\PT0.txt

Output Set: N:\CRF3\02052001\I623746.raw

L:2095 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (107) SEQUENCE:
 L:2098 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2099 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (108) SEQUENCE:
 L:2142 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2143 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (110) SEQUENCE:
 L:2251 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2252 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (115) SEQUENCE:
 L:2445 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2446 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (125) SEQUENCE:
 L:2449 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2450 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (126) SEQUENCE:
 L:2453 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2454 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (127) SEQUENCE:
 L:2725 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2726 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (138) SEQUENCE:
 L:2967 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2968 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (150) SEQUENCE:
 L:2971 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2972 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (151) SEQUENCE:
 L:3002 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3003 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (153) SEQUENCE:
 L:3223 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3224 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (166) SEQUENCE:
 L:3227 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3228 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (167) SEQUENCE:
 L:3360 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3361 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (174) SEQUENCE:
 L:3364 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3365 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (175) SEQUENCE:
 L:3368 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3369 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (176) SEQUENCE:
 L:3789 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:4174 M:254 E: No. of Bases conflict, LENGTH:Input:960 Counted:959 SEQ:220
 M:254 Repeated in SeqNo-220
 L:4212 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3210 Found:3209 SEQ:220
 L:4439 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:227
 L:4439 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:227
 L:4439 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:227
 L:4439 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:227
 L:4439 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:227
 L:5009 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:241
 L:5009 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:241
 L:5009 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:241
 L:5009 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:241
 L:5009 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:241
 L:5010 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:241
 L:5010 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:241
 L:5010 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:241
 L:5010 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:241

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/623,746

DATE: 02/05/2001

TIME: 16:30:28

Input Set : A:\PTO.txt

Output Set : N:\CRF3\02052001\I623746.raw

M:340 Repeated in SeqNo=241

L:5050 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:243

L:5050 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:243

L:5050 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:243

L:5050 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:243

L:5050 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:243

L:5051 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:243

L:5051 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:243

L:5051 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:243

L:5051 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:243

M:340 Repeated in SeqNo=243

L:5054 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:243

L:5054 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:243

L:5054 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:243

L:5054 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:243

L:5055 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:243

L:5055 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:243

L:5055 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:243

L:5055 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:243

L:5056 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:243

L:5056 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:243

L:6017 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:6081 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

L:7073 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3

L:7076 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4

L:7079 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3

L:7082 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6

L:7085 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2

L:7094 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4

L:7097 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4

L:7100 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2

L:7103 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7

L:7106 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5